

SEQUENCE LISTING

<110> Genencor International, Inc.
 Fox, Judith A.
 Harding, Fiona A.
 Schellenberger, Volker

<120> CAB Molecules

<130> GC822-PCT

<140> PCT/US2004/041429

<141> 2004-12-10

<150> US 60/529,354

<151> 2003-12-12

<150> US 60/577,255

<151> 2004-04-06

<160> 133

<170> PatentIn version 3.2

<210> 1

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRs of CAB1 protein

<220>

<221> MISC_FEATURE

<222> (1)..(25)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (36)..(49)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (66)..(98)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (110)..(158)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (169)..(183)

<223> X = any amino acid

<220>

<221> MISC_FEATURE

<222> (191)..(222)

<223> X = any amino acid

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Ser Asn Leu Ala Ser Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195	200	205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln		
210	215	220
Arg Ser Ser Tyr Pro Leu Thr		
225	230	
<210> 2		
<211> 605		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> CAB1 protein		
<400> 2		
Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr		
1	5	10 15
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser		
	20	25 30
Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile		
	35	40 45
Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe		
	50	55 60
Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr		
65	70	75 80
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90 95
Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln		
	100	105 110
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly		
	115	120 125
Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala		
	130	135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro

370						375										380
Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	Tyr	Ala	Asn	Ala	Ser	Ile	Gly	
385						390				395					400	
Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	Ser	Gly	Met	Pro	Tyr	Glu	Gln	
				405					410					415		
Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	Leu	Lys	Leu	Asp	His	Thr	Trp	
			420					425					430			
Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	His	Tyr	Ala	Trp	Gly	Tyr	Arg	
	435						440					445				
Asp	Gly	Lys	Ala	Val	Arg	Val	Ser	Pro	Gly	Met	Leu	Asp	Ala	Gln	Ala	
	450					455					460					
Tyr	Gly	Val	Lys	Thr	Asn	Val	Gln	Asp	Met	Ala	Asn	Trp	Val	Met	Ala	
465					470					475					480	
Asn	Met	Ala	Pro	Glu	Asn	Val	Ala	Asp	Ala	Ser	Leu	Lys	Gln	Gly	Ile	
				485					490					495		
Ala	Leu	Ala	Gln	Ser	Arg	Tyr	Trp	Arg	Ile	Gly	Ser	Met	Tyr	Gln	Gly	
			500					505					510			
Leu	Gly	Trp	Glu	Met	Leu	Asn	Trp	Pro	Val	Glu	Ala	Asn	Thr	Val	Val	
	515						520					525				
Glu	Thr	Ser	Phe	Gly	Asn	Val	Ala	Leu	Ala	Pro	Leu	Pro	Val	Ala	Glu	
	530					535					540					
Val	Asn	Pro	Pro	Ala	Pro	Pro	Val	Lys	Ala	Ser	Trp	Val	His	Lys	Thr	
545					550					555					560	
Gly	Ser	Thr	Gly	Gly	Phe	Gly	Ser	Tyr	Val	Ala	Phe	Ile	Pro	Glu	Lys	
			565						570					575		
Gln	Ile	Gly	Ile	Val	Met	Leu	Ala	Asn	Thr	Ser	Tyr	Pro	Asn	Pro	Ala	
		580						585					590			
Arg	Val	Glu	Ala	Ala	Tyr	His	Ile	Leu	Glu	Ala	Leu	Gln				
	595						600					605				

<210> 3
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> BLA protein

<400> 3

Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile
1 5 10 15

Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met Ala Val Ala Val
20 25 30

Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile
35 40 45

Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser
50 55 60

Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
65 70 75 80

Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu
85 90 95

Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr
100 105 110

Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn
115 120 125

Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro
130 135 140

Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala
145 150 155 160

Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr
165 170 175

Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro

180	185	190
Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala		
195	200	205
Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys		
210	215	220
Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala Asn Met Ala Pro		
225	230	235
Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln		
245	250	255
Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu		
260	265	270
Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe		
275	280	285
Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro		
290	295	300
Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly		
305	310	315
Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile		
325	330	335
Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala		
340	345	350
Ala Tyr His Ile Leu Glu Ala Leu Gln		
355	360	

<210> 4
 <211> 3
 <212> PRT
 <213> Unknown

 <220>
 <223> skipped

 <400> 4

Ala Ala Ala

1

<210> 5
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRs of CAB1.6 protein variant

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (66)..(98)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (110)..(158)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (169)..(183)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (191)..(222)
<223> X = any amino acid

<400> 5

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Leu Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr
225 230

<210> 6

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRs of CAB1.7 protein variant

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (66)..(98)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (110)..(158)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (169)..(183)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (191)..(222)
<223> X = any amino acid

<400> 6

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Phe	Asn	Ile	Lys	Asp	Ser
			20					25					30		

Tyr	Met	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35						40				45			

Xaa	Trp	Ile	Asp	Pro	Glu	Asn	Gly	Asp	Thr	Glu	Tyr	Ala	Pro	Lys	Phe
	50					55					60				

Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75						80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85				90						95	

Xaa	Xaa	Gly	Leu	Pro	Leu	Gly	Ala	Ile	Tyr	Asn	Asp	Tyr	Xaa	Xaa	Xaa
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100	105	110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
115	120	125
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
130	135	140
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala		
145	150	155 160
Ser Ser Ala Val Tyr Ala Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
165	170	175
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa		
180	185	190
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
195	200	205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln		
210	215	220
Arg Asp Ser Tyr Pro Leu Thr		
225	230	

<210> 7
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CAB 1.6 protein variant

<400> 7

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30
Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly

275					280					285					
Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	Val	Thr	Pro	Gln	Thr	Leu	Phe
290						295					300				
Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	Thr	Gly	Val	Leu	Gly	Gly	Asp
305					310					315					320
Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu	Asp	Asp	Ala	Val	Thr	Arg	Tyr
				325					330					335	
Trp	Pro	Gln	Leu	Thr	Gly	Lys	Gln	Trp	Gln	Gly	Ile	Arg	Met	Leu	Asp
			340					345					350		
Leu	Ala	Thr	Tyr	Thr	Ala	Gly	Gly	Leu	Pro	Leu	Gln	Val	Pro	Asp	Glu
		355					360					365			
Val	Thr	Asp	Asn	Ala	Ser	Leu	Leu	Arg	Phe	Tyr	Gln	Asn	Trp	Gln	Pro
	370					375					380				
Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	Tyr	Ala	Asn	Ala	Ser	Ile	Gly
385					390					395					400
Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	Ser	Gly	Met	Pro	Tyr	Glu	Gln
				405					410					415	
Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	Leu	Lys	Leu	Asp	His	Thr	Trp
			420					425					430		
Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	His	Tyr	Ala	Trp	Gly	Tyr	Arg
		435					440					445			
Asp	Gly	Lys	Ala	Val	Arg	Val	Ser	Pro	Gly	Met	Leu	Asp	Ala	Gln	Ala
	450					455					460				
Tyr	Gly	Val	Lys	Thr	Asn	Val	Gln	Asp	Met	Ala	Asn	Trp	Val	Met	Ala
465					470					475					480
Asn	Met	Ala	Pro	Glu	Asn	Val	Ala	Asp	Ala	Ser	Leu	Lys	Gln	Gly	Ile
				485				490						495	
Ala	Leu	Ala	Gln	Ser	Arg	Tyr	Trp	Arg	Ile	Gly	Ser	Met	Tyr	Gln	Gly
			500					505					510		

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 8
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.6i protein variant

<400> 8

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85								90				95			
Asn	Glu	Gly	Leu	Pro	Thr	Gly	Pro	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln
			100								105			110	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			115										125		
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Asn	Val	Leu	Thr	Gln	Ser	Pro	Ala
			130									140			
Ile	Val	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala
							150					155			160
Ser	Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr
							165							175	
Ser	Pro	Lys	Leu	Val	Ile	Tyr	Asp	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val
							180							190	
Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr
							195							205	
Ile	Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
							210							220	
Arg	Asp	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu
							225							235	240
Lys	Arg	Ala	Ala	Thr	Pro	Val	Ser	Glu	Lys	Gln	Leu	Ala	Glu	Val	Val
							245							255	
Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Ala	Ala	Gln	Ser	Val	Pro	Gly	Met
							260							270	
Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	Pro	His	Tyr	Tyr	Thr	Phe	Gly
							275							285	
Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	Val	Thr	Pro	Gln	Thr	Leu	Phe
							290							300	
Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	Thr	Gly	Val	Leu	Gly	Gly	Asp
							305							315	320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 9
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.7 protein variant

<400> 9

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Asp Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 10
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.7i protein variant

<400> 10

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Lys Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 protein fragment

<400> 11

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
 225 230 235 240

Lys Arg Ala Ala

<210> 12
 <211> 5178
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic pME27.1 plasmid sequence

<400> 12
 aggaattatc atatgaaata cctgctgccg accgctgctg ctgggtctgct gctcctcgtc 60
 gccacgccgg ccatggccca ggtgaaactg cagcagctctg gggcagaact tgtgaggtca 120
 gggacctcag tcaagttgtc ctgcacagct tctggcttca acattaaaga ctccctatatg 180
 cactgggttga ggcagggggc tgaacagggc ctggagtgga ttggatggat tgatcctgag 240
 aatggtgata ctgaatatgc cccgaagtgc cagggcaagg ccacttttac tacagacaca 300
 tctccaaca cagcctacct gcagctcagc agcctgacat ctgaggacac tgccgtctat 360
 tattgtaatg aggggactcc gactggggccg tactactttg actactgggg ccaagggcdc 420
 acggtcaccg tctcctcagg tggaggcggg tcaggcggag gtggctctgg cgggtggcgga 480
 tcagaaaatg tgctcaccca gtctccagca atcatgtctg catctccagg ggagaaggtc 540
 accataacct gcagtgccag ctcaagtgtg agttacatgc actggttcca gcagaagcca 600
 ggcacttctc ccaaactctg gatattatagc acatccaacc tggtttcttg agtccttctg 660
 cgcttcagtg gcagtggatc tgggacctct tactctctca caatcagccg aatggaggct 720
 gaagatgctg ccacttatta ctgccagcaa agatctagtt acccactcac gttcggtgct 780
 ggcaccaagc tggagctgaa acgggcgggc acaccgggtg cagaaaaaca gctggcgagg 840
 gtggtcgcga atacgattac cccgtgatg aaagcccagt ctgttccagg catggcggtg 900
 gccgttattt atcagggaaa accgcactat tacacatttg gcaaggccga tatcgcgggc 960

aataaaccgc	ttacgcctca	gaccctgttc	gagctgggtt	ctataagtaa	aaccttcacc	1020
ggcgtttttag	gtgggggatgc	cattgctcgc	ggtgaaat	cgctggacga	tgcggtgacc	1080
agatactggc	cacagctgac	gggcaagcag	tggcagggta	ttcgtatgct	ggatctcgcc	1140
acctacaccg	ctggcggcct	gccgctacag	gtaccggatg	aggtcacgga	taacgcctcc	1200
ctgctgcgct	tttatcaaaa	ctggcagccg	cagtggaagc	ctggcacaac	gcgtctttac	1260
gccaacgcc	gcatcggtct	ttttggtgcg	ctggcggtca	aaccttctgg	catgccttat	1320
gagcaggcca	tgacgacgcg	ggtccttaag	ccgctcaagc	tggaccatac	ctggattaac	1380
gtgccgaaag	cggaagaggc	gcattacgcc	tggggctatc	gtgacggtaa	agcgggtgcgc	1440
gtttcgccgg	gtatgctgga	tgcacaagcc	tatggcgtga	aaaccaacgt	gcaggatatg	1500
gcgaactggg	tcattggcaa	catggcgccg	gagaacgttg	ctgatgcctc	acttaagcag	1560
ggcatcgcg	tggcgcgctc	gcgctactgg	cgtatcgggg	caatgtatca	gggtctgggc	1620
tgggagatgc	tcaactggcc	cgtggaggcc	aacacgggtg	tcgagacgag	ttttggtaat	1680
gtagcactgg	cgccgttgcc	cgtggcagaa	gtgaatccac	cggtccccc	ggtcaaagcg	1740
tcttgggtcc	ataaaacggg	ctctactggc	gggtttggca	gctacgtggc	ctttattcct	1800
gaaaagcaga	tcggtattgt	gatgctcgcg	aatacaagct	atccgaaccc	ggcacgcgtt	1860
gaggcgcat	accatatact	cgaggcgcta	cagtaggaat	tcgagctccg	tcgacaagct	1920
tgcggccgca	ctcgagatca	aacgggctag	ccagccagaa	ctcgccccgg	aagaccccga	1980
ggatgtcgag	caccaccacc	accaccactg	agatccggct	gctaacaaag	cccgaaagga	2040
agctgagttg	gctgctgcc	ccgctgagca	ataactagca	taacccttg	gggcctctaa	2100
acgggtcttg	aggggttttt	gctgaaagga	ggaactatat	ccggattggc	gaatgggacg	2160
cgccctgtag	cggcgcatta	agcgcgcgcg	gtgtggtggt	tacgcgcagc	gtgaccgcta	2220
cacttgccag	cgccctagcg	cccgtcctt	tcgctttctt	cccttccttt	ctcgccacgt	2280
tcgcccgtt	tccccgtcaa	gctctaaatc	gggggctccc	tttagggttc	cgatttagtg	2340
ctttacggca	cctcgacccc	aaaaaacttg	attaggggtga	tggttcacgt	agtgggccat	2400
cgccctgata	gacgggtttt	cgccctttga	cgttgagtc	cacgttcttt	aatagtggac	2460
tcttgttcca	aactggaaca	acactcaacc	ctatctcggt	ctattctttt	gatttataag	2520
ggattttgcc	gatttcggcc	tattggttaa	aaaatgagct	gatttaacaa	aaatttaacg	2580
cgaattttta	caaaatatta	acgcttacia	tttctgatg	cggtattttc	tccttacgca	2640
tctgtgcggt	atttcacacc	gcatatggtg	cactctcagt	acaatctgct	ctgatgccgc	2700

atagttaagc cagccccgac acccgccaac acccgctgac gcgccctgac gggcttgtct	2760
gctcccggca tccgcttaca gacaagctgt gaccgtctcc gggagctgca tgtgtcagag	2820
gttttcaccg tcatcaccga aacgcgcgag acgaaagggc ctcgatgatac gcctatTTTT	2880
ataggTTaat gtcatgataa taatggTTTT ttagacgtca ggtggcactt ttcggggaaa	2940
tgtgcgcgga acccctatTT gtTTatTTTT ctAAatacat tcaaatatgt atccgctcat	3000
gagacaataa ccctgtggca gcatcaccgc acgcactTTg cgccgaataa atacctgtga	3060
cggaagatca cttcgcagaa taaataaatc ctggtgtccc tgttgatacc gggaagccct	3120
gggccaaactt ttggcgaaaa tgagacgttg atcggcacgt aagaggTTcc aactttcacc	3180
ataatgaaat aagatcacta ccgggcgtat tttttgagtt atcgagattt tcaggagcta	3240
aggaagctaa aatggagaaa aaaatcactg gatataccac cgttgatata tcccaatggc	3300
atcgtaaaga acatTTtgag gcatttcagt cagttgctca atgtacctat aaccagaccg	3360
ttcagctgga tattacggcc tttttaaaga ccgtaaagaa aaataagcac aagTTTTatc	3420
cggcctTTat tcacattctt gccgcctga tgaatgctca tccggaattc cgtatggcaa	3480
tgaagacgg tgagctggtg atatgggata gtgttcaccc ttgttacacc gttttccatg	3540
agcaaactga aacgtTTTca tcgctctgga gtgaatacca cgacgatttc cggcagTTtc	3600
tacacatata ttcgcaagat gtggcgtggt acggtgaaaa cctggcctat ttccctaaag	3660
ggTTTTattga gaatatgTTt ttcgctctcag ccaatccctg ggtgagTTtc accagTTTTg	3720
atttaaacgt ggccaatatg gacaacttct tcgccccgt tttcacgatg ggcaaattt	3780
atacgcaagg cgacaaggTg ctgatgccgc tggcgattca ggttcatcat gccgtctgtg	3840
atggcttcca tgtcggcaga atgcttaatg aattacaaca gtactgcat gatggcagg	3900
gcggggcgta aagacagatc gctgagatag gtgcctcact gattaagcat tggtaactgt	3960
cagaccaagt ttactcatat atactTTtaga ttgattTaaa acttcatttt ttaattTaaa	4020
aggatctagg tgaagatcct ttttgataat ctcatgacca aaatccctta acgtgagTTt	4080
tcgttccact gagcgtcaga ccccgtagaa aagatcaaag gatcttcttg agatcctttt	4140
tttctgcgcg taatctgctg cttgcaaaca aaaaaaccac cgctaccagc ggtggTTTTgt	4200
ttgccggatc aagagctacc aactctTTTT ccgaaggtaa ctggcttcag cagagcgcag	4260
ataccaaata ctgttcttct agtgtagccg tagttaggcc accacttcaa gaactctgta	4320
gcaccgccta catacctcgc tctgctaatc ctgttaccag tggctgctgc cagtggcgat	4380

```

aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac cggataaggc gcagcgggtcg 4440
ggctgaacgg ggggttcgtg cacacagccc agcttggagc gaacgaccta caccgaactg 4500
agatacctac agcgtgagct atgagaaagc gccacgcttc ccgaagggag aaaggcggac 4560
aggatatccg taagcggcag ggtcggaaca ggagagcgca cgaggagct tccaggggga 4620
aacgcctggt atctttatag tctgtcggg tttcgccacc tctgacttga gcgtcgattt 4680
ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg ccagcaacgc ggccttttta 4740
cggttcctgg ccttttgctg gccttttgct cacatgttct ttctgcgtt atcccctgat 4800
tctgtggata accgtattac cgcctttgag tgagctgata ccgctcgccg cagccgaacg 4860
accgagcgca gcgagtcagt gagcgaggaa gcggaagagc gcccaatacg caaacgcct 4920
ctccccgcgc gttggccgat tcattaatgc agctggcagc acaggtttcc cgactggaaa 4980
gcgggcagtg agcgcaacgc aattaatgtg agttagctca ctcattaggc accccaggct 5040
ttacacttta tgcttcggc tcgtatgttg tgtggaattg tgagcggata acaatttcac 5100
acaggaaaca gctatgacca tgattacgcc aagctattta ggtgacacta tagaatactc 5160
aagctttcta gattaagg 5178

```

```

<210> 13
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 heavy chain sequence

<400> 13

```

```

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr
1          5          10          15

```

```

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
          20          25          30

```

```

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
          35          40          45

```

```

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
          50          55          60

```

```

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65          70          75          80

```

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 linker sequence

<400> 14

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 15
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 light chain sequence

<400> 15

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Ala Thr
100 105 110

<210> 16
<211> 360
<212> PRT
<213> Artificial Sequence

<220>
<223> BLA protein fragment

<400> 16

Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr
1 5 10 15

Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met Ala Val Ala Val Ile
20 25 30

Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala
35 40 45

Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile
50 55 60

Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly
65 70 75 80

Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr
85 90 95

Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr
100 105 110

Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala
115 120 125

Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly
130 135 140

Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu
145 150 155 160

Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg
165 170 175

Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys
180 185 190

Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val
195 200 205

Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr
210 215 220

Asn Val Gln Asp Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu
225 230 235 240

Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser
245 250 255

Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met
260 265 270

Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly
275 280 285

Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala
290 295 300

Pro Pro Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly
305 310 315 320

Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val
325 330 335

Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala
340 345 350

Tyr His Ile Leu Glu Ala Leu Gln
355 360

<210> 17
<211> 605
<212> PRT

<213> Artificial Sequence

<220>

<223> SW149.5 protein

<400> 17

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 18
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.1 protein variant

<400> 18

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Val Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 19
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> CAB1.2 variant coding sequence

<400> 19
caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
tcctgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatgggtga tactgaatat 180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgagggggact 300
ccgactgggc cgtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca 360

ggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgctgctacc	420
cagtctccag caatcgtgtc tgcattctcca ggggagaagg tcaccataac ctgcagtgcc	480
agctcaagtg taagttacat gcactgggtc cagcagaagc caggcacttc tcccaaactc	540
gtgatttata gcacatccaa cctggcttct ggagtccttg ctcgcttcag tggcagtgga	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgccagc aaagatctag ttaccactc acgttcggtg ctggcaccaa gctggagctg	720
aaacgggchg ccacaccggt gtcagaaaaa cagctggchg aggtggctcg gaatacgatt	780
accccgctga tgaaagccca gtctgttcca ggcatggchg tggcgttat ttatcaggga	840
aaaccgcact attacacatt tggcaaggcc gatatcgchg cgaataaacc cgttacgct	900
cagacctgt tcgagctggg ttctataagt aaaaccttca ccggcgtttt aggtggggat	960
gccattgctc gcggtgaaat ttcgctggac gatcgggtga ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtcacg gataacgcct ccctgctgch cttttatcaa	1140
aactggcagc cgcagtggaa gcctggcaca acgctcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggacat acctggatta acgtgccga agcggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcggctg gcgtttcgcc gggatatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca	1440
aacatggchg cggagaacgt tgctgatgcc tactttaagc agggcatcgc gctggcgch	1500
tcgcgctact ggcgtatcgg gtcaatgtat cagggtctgg gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggt atgtagcact ggcgccgttg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaacg	1680
ggctctactg gcgggtttgg cagctacgtg gcctttattc ctgaaaagca gatcggatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgch ttgaggcggc ataccatatc	1800
ctcgaggchg tacag	1815

<210> 20
 <211> 605
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> CAB1.2 protein variant

<400> 20

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln

210						215						220					
Arg	Ser	Ser	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu		
225					230					235					240		
Lys	Arg	Ala	Ala	Thr	Pro	Val	Ser	Glu	Lys	Gln	Leu	Ala	Glu	Val	Val		
				245					250					255			
Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Lys	Ala	Gln	Ser	Val	Pro	Gly	Met		
			260					265					270				
Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	Pro	His	Tyr	Tyr	Thr	Phe	Gly		
		275					280					285					
Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	Val	Thr	Pro	Gln	Thr	Leu	Phe		
	290					295					300						
Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	Thr	Gly	Val	Leu	Gly	Gly	Asp		
305					310					315					320		
Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu	Asp	Asp	Ala	Val	Thr	Arg	Tyr		
				325					330					335			
Trp	Pro	Gln	Leu	Thr	Gly	Lys	Gln	Trp	Gln	Gly	Ile	Arg	Met	Leu	Asp		
			340					345					350				
Leu	Ala	Thr	Tyr	Thr	Ala	Gly	Gly	Leu	Pro	Leu	Gln	Val	Pro	Asp	Glu		
		355					360					365					
Val	Thr	Asp	Asn	Ala	Ser	Leu	Leu	Arg	Phe	Tyr	Gln	Asn	Trp	Gln	Pro		
	370					375					380						
Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	Tyr	Ala	Asn	Ala	Ser	Ile	Gly		
385					390					395					400		
Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	Ser	Gly	Met	Pro	Tyr	Glu	Gln		
				405					410					415			
Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	Leu	Lys	Leu	Asp	His	Thr	Trp		
			420					425					430				
Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	His	Tyr	Ala	Trp	Gly	Tyr	Arg		
	435						440					445					

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 21

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRs of CAB1.4 protein variant

<220>

<221> MISC_FEATURE

<222> (1)..(25)

<223> X = any amino acid

<220>

<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (66)..(98)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (110)..(158)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (169)..(183)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (191)..(222)
<223> X = any amino acid

<400> 21

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Phe	Asn	Ile	Lys	Asp	Ser
			20					25					30		

Tyr	Met	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35						40					45		

Xaa	Trp	Ile	Asp	Pro	Glu	Asn	Gly	Asp	Thr	Glu	Tyr	Ala	Pro	Lys	Phe
	50					55					60				

Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75					80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Gly	Thr	Pro	Thr	Gly	Pro	Tyr	Tyr	Phe	Asp	Tyr	Xaa	Xaa	Xaa
			100					105					110		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			115				120					125			

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr
225 230

<210> 22
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CDRs of CAB1.4 variant

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

<400> 22
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnggcttca acattaaaga ctctatatg 180
cacnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnntggat tgatcctgag 240
aatggtgata ctgaatatgc cccgaagttc cagnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nngggactcc gactgggccg tactactttg actacnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnagtgccag ctcaagtgtg agttacatgc acnnnnnnnn nnnnnnnnnn 600
nnnnnnnnnn nnnnnnnnnn nnnnnnngat acatccaacc tggcttctnn nnnnnnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnnn nnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 23
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CAB1.4 variant

<400> 23
caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
tcctgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
cctgaacagg gcttgaggatg gattggatgg attgatcctg agaatggtga tactgaatat 180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgagggggact 300

ccgactgggc	cgtactactt	tgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggtggaggcg	gttcaggcgg	aggtggctct	ggcgggtggcg	gatcagaaaa	tgtgctcacc	420
cagtctccag	caatcgtgtc	tgcatctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcaagtg	taagttacat	gcactggttc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttatg	atacatccaa	cctggcttct	ggagtccttg	ctcgcttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagagatag	ttaccctctc	acgttcggtg	ctggcaccaa	gctggagctg	720
aaacgggcgg	ccacaccggg	gtcagaaaaa	cagctggcgg	aggtggtcgc	gaatacgatt	780
accccgctga	tgaaagccca	gtctgttcca	ggcatggcgc	tggccgttat	ttatcaggga	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
cagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgatatg	ctggatctcg	ccacctacac	cgtggcgggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	ccctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaacgc	cagcatcggt	1200
ctttttggtg	cgtggcgggt	caaaccttct	ggcatgccct	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcgggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggg	aaagcgggtgc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggtcatggca	1440
aacatggcgc	cggagaacgt	tgctgatgcc	tcacttaagc	agggcatcgc	gctggcgag	1500
tcgcgctact	ggcgtatcgg	gtcaatgtat	cagggctctgg	gctgggagat	gctcaactgg	1560
cccgtggagg	ccaacacggg	ggtcgagacg	agttttggta	atgtagcact	ggcgccgttg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccggcctaaag	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcggggttgg	cagctacgtg	gcctttattc	ctgaaaagca	gatcgggtatt	1740
gtgatgctcg	cgaatacaag	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatatc	1800
ctcgaggcgc	tacag					1815

<210> 24
 <211> 605
 <212> PRT

<213> Artificial Sequence

<220>

<223> CAB1.4 protein variant

<400> 24

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 25
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CDRs of CAB1.6 variant

<220>
<221> misc_feature
<222> (1)..(153)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (184)..(225)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (274)..(372)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (406)..(552)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (583)..(627)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (649)..(744)

<223> n = a,t,c, or g

<400> 25

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnggcttca acattaaaga ctctatatg 180

cacnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnntggat tgatcctgag 240

aatggtgata ctgaatatgc cccgaagttc cagnnnnnnn nnnnnnnnnn nnnnnnnnnn 300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360

nnnnnnnnnn nngggctccc gactgggccc tactactttg actacnnnnn nnnnnnnnnn 420

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540

nnnnnnnnnn nnagtgccag ctcaagtgtg agttacatgc acnnnnnnnn nnnnnnnnnn 600

nnnnnnnnnn nnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnn nnnnnnnnnn 660

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720

nnnnnnnnnn nnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 26

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence encoding CAB1.6 protein variant

<400> 26

caggtgcagc	tgcagcagtc	tggggcagaa	cttgtgaaat	cagggggctc	agtcaagttg	60
tcttgcacag	cttctggctt	caacattaaa	gactcctata	tgcactgggt	gaggcagggg	120
cctgaacagg	gcctggagtg	gattggatgg	attgatcctg	agaatgggtga	tactgaatat	180
gccccgaagt	tccagggcaa	ggccactttt	actacagaca	catcctccaa	cacagcctac	240
ctgcagctca	gcagcctgac	atctgaggac	actgccgtct	attattgtaa	tgagggggctc	300
ccgactgggc	cgtactactt	tgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggtagggg	ggtcaggcgg	aggtggctct	ggcggtaggg	gatcagaaaa	tgtcgtcacc	420
cagtctccag	caatcgtgtc	tgcatctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcaagtg	taagttacat	gcactgggtc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttatg	atacatccaa	cctggcttct	ggagtccttg	ctcgtttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagagatag	ttaccctctc	acgttcgggtg	ctggcaccaa	gctggagctg	720
aaacgggcgg	ccacaccggg	gtcagaaaaa	cagctggcgg	aggtggtcgc	gaatacgatt	780
accccgctga	tgaaagccca	gtctgttcca	ggcatggcgg	tggccgttat	ttatcagggg	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
cagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcgggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgtatg	ctggatctcg	ccacctacac	cgctggcggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	cctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaacgc	cagcatcggt	1200
ctttttggtg	cgctggcggt	caaaccttct	ggcatgcctt	atgagcaggg	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggg	aaagcgggtgc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggatcatggca	1440
aacatggcgc	cggagaacgt	tgctgatgcc	tcacttaagc	agggcatcgc	gctggcgag	1500

tccgcgtact	ggcgtatcgg	gtcaatgtat	caggggtctgg	gctgggagat	gctcaactgg	1560
cccgtggagg	ccaacacggt	ggtcgagacg	agttttggta	atgtagcact	ggcgccgttg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccgggtcaaag	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcggttttgg	cagctacgtg	gcctttattc	ctgaaaagca	gatcgggtatt	1740
gtgatgctcg	cgaatacaag	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatata	1800
ctcgaggcgc	tacag					1815

<210> 27
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.6i protein variant

<400> 27	
caggtgcagc	60
tgcagcagtc	
tggggcagaa	
cttgtgaaat	
cagggggctc	
agtcaagttg	
tccctgcacag	120
cttctggctt	
caacattaaa	
gactcctata	
tgcactgggt	
gaggcagggg	
cctgaacagg	180
gacctggagt	
gattggatgg	
attgatcctg	
agaatgggtga	
tactgaatat	
gccccgaagt	240
tccagggcaa	
ggccactttt	
actacagaca	
catcctccaa	
cacagcctac	
ctgcagctca	300
gcagcctgac	
atctgaggac	
actgccgtct	
attattgtaa	
tgaggggctc	
ccgactgggc	360
cgtactactt	
tgactactgg	
ggccaaggga	
ccacgggtcac	
cgtctcctca	
ggcggaggcg	420
gttcaggcgg	
aggtggctct	
ggcgggtggcg	
gatcagaaaa	
tgtgctcacc	
cagtctccag	480
caatcgtgtc	
tgcattctcca	
ggggagaagg	
tcaccataac	
ctgcagtgcc	
agctcaagtg	540
taacttacat	
gcactgggtc	
cagcagaagc	
caggcacttc	
tcccaaactc	
gtgatttatg	600
atacatccaa	
cctggcttct	
ggagtcctct	
ctcgcttcag	
tggcagtgga	
tctgggacct	660
cttactctct	
cacaatcagc	
cgaatggagg	
ctgaagatgc	
tgccacttat	
tactgccagc	720
aaagagatag	
ttaccacttc	
acgttcgggt	
ctggcaccaa	
gctggagctg	
aaacgggcgg	780
ccacaccggt	
gtcagaaaaa	
cagctggcgg	
aggtgggtcgc	
gaatacgatt	
accccgtga	840
tggcggccca	
gtctgttcca	
ggcatggcgg	
tggccgttat	
ttatcagggg	
aaaccgcact	900
attacacatt	
tggcaaggcc	
gatatcgcgg	
cgaataaacc	
cgttacgcct	
cagacctgt	960
tcgagctggg	
ttctataagt	
aaaaccttca	
ccggcgtttt	
aggtggggat	
gccattgctc	1020
gcggtgaaat	
ttcgctggac	
gatgcgggtga	
ccagatactg	
gccacagctg	
acgggcaagc	1080
agtggcaggg	
tattcgtatg	
ctggatctcg	
ccacctacac	
cgctggcggc	

```

ctgccgctac aggtaccgga tgaggtcacg gataacgcct ccctgctgcg cttttatcaa 1140
aactggcagc cgcagtgga gctggcaca acgcgtcttt acgccaacgc cagcatcggt 1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg 1260
cgggtcctta agccgctcaa gctggacat acctggatta acgtgccgaa agcggaagag 1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtgc gcgtttcgcc gggatatgctg 1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca 1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgcag 1500
tcgcgctact ggcgtatcgg gtcaatgtat caggggtctgg gctgggagat gctcaactgg 1560
cccgtggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgccgttg 1620
ccctgggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaacg 1680
ggctctactg gcggggttgg cgcgtacgtg gcctttattc ctgaaaagca gatcgggtatt 1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata 1800
ctcgaggcgc tacag 1815

```

```

<210> 28
<211> 771
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding CDRs of CAB1.7 protein variant

```

```

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

```

<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

<400> 28
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnggcttca acattaaaga ctctatatg 180
cacnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnntggat tgatcctgag 240
aatggtgata ctgaatatgc cccgaagttc cagnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nngggctccc gctcggggcc atttacaacg actacnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnagtgccag ctgagctgta tatgccatgc acnnnnnnnn nnnnnnnnnn 600
nnnnnnnnnn nnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnn nnnnnnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnnn nnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 29
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CAB1.7 protein variant

<400> 29
caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
tcctgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggtga tactgaatat 180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgagggggctc 300

ccgctcgggg	ccatttacia	cgactactgg	ggccaaggga	ccacgggtcac	cgtctcctca	360
ggtggaggcg	gttcaggcgg	aggtggctct	ggcgggtggcg	gatcagaaaa	tgtgctcacc	420
cagtctccag	caatcgtgtc	tgcactctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcagctg	tatatgccat	gcactgggtc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttatg	atacatccaa	cctggcttct	ggagtccttg	ctcgcttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagagatag	ttaccactc	acgttcgggtg	ctggcaccaa	gctggagctg	720
aaacgggcg	ccacaccgg	gtcagaaaaa	cagctggcgg	aggtggtcgc	gaatacgatt	780
accccgctga	tgaaagccca	gtctgttcca	ggcatggcgg	tggcggttat	ttatcaggga	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
cagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcgggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgtatg	ctggatctcg	ccacctacac	cgctggcggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	cctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaacgc	cagcatcggt	1200
ctttttggtg	cgctggcggt	caaaccttct	ggcatgcctt	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggt	aaagcgggtgc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggtcatggca	1440
aacatggcgc	cggagaacgt	tgtgatgccc	tcacttaagc	agggcatcgc	gctggcgag	1500
tcgcgctact	ggcgtatcgg	gtcaatgtat	caggggtctgg	gctgggagat	gctcaactgg	1560
cccgtggagg	ccaacacgg	ggtcgagacg	agttttggta	atgtagcact	ggcgccggtg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccgggtcaaag	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcgggttttg	cagctacgtg	gcctttattc	ctgaaaagca	gatcggtatt	1740
gtgatgctcg	cgaatacaag	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatata	1800
ctcgaggcgc	tacag					1815

<210> 30
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>

<223> sequence encoding CAB1.7i protein variant

<400> 30

caggtgcagc	tgcagcagtc	tggggcagaa	cttgtgaaat	cagggggctc	agtcaagttg	60
tcttgcacag	cttctggctt	caacattaaa	gactcctata	tgcactgggt	gaggcagggg	120
cctgaacagg	gcctggagtg	gattggatgg	attgatcctg	agaatgggtga	tactgaatat	180
gccccgaagt	tccagggcaa	ggccactttt	actacagaca	catcctccaa	cacagcctac	240
ctgcagctca	gcagcctgac	atctgaggac	actgccgtct	attattgtaa	tgaggggctc	300
ccgctcgggg	ccattttaaa	cgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggcggaggcg	gttcaggcgg	aggtggctct	ggcgggtggc	gatcagaaaa	tgtgctcacc	420
cagtctccag	caatcgtgtc	tgcattctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcagctg	tatatgccat	gcactgggtc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttatg	atacatccaa	cctggcttct	ggagtcctct	ctcgcttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagagatag	ttaccctctc	acgttcggtg	ctggcaccaa	gctggagctg	720
aaacgggcgg	ccacaccggc	gtcagaaaaa	cagctggcgg	aggtggctgc	gaatacgatt	780
accccgctga	tggcggccca	gtctgttcca	ggcatggcgg	tggccgttat	ttatcagggg	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
cagaccctgt	tgcagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcgggtgaaat	ttcgctggac	gatgcgggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgtatg	ctggatctcg	ccacctacac	cgctggcggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	ccctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaaacg	cagcatcggt	1200
ctttttggtg	cgctggcggc	caaaccttct	ggcatgccct	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcgggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggc	aaagcgggtg	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggcatgagca	1440
aacatggcgc	cggagaacgt	tgtgatgcc	tcacttaagc	agggcatcgc	gctggcgag	1500
tcgcgctact	ggcgtatcgg	gtcaatgtat	cagggctctgg	gctgggagat	gctcaactgg	1560

```

cccggtggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgcggttg 1620
cccggtggcag aagtgaatcc accgggtccc ccggtcaaag cgtcctgggt ccataaaacg 1680
ggctctactg gcggggtttg cgcgtagctg gcctttattc ctgaaaagca gatcggtatt 1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata 1800
ctcgaggcgc tacag 1815

```

```

<210> 31
<211> 771
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding CDRs of CAB1 protein

```

```

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

```

```

<400> 31
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnggcttca acattaaaga ctccatatg 180

```

cacnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnntggat tgatectgag	240
aatggtgata ctgaatatgc cccgaagtgc cagnnnnnnn nnnnnnnnnn nnnnnnnnnn	300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	360
nnnnnnnnnn nngggactcc gactgggccc tactactttg actacnnnnn nnnnnnnnnn	420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	540
nnnnnnnnnn nnagtgccag ctcaagtgtg agttacatgc acnnnnnnnn nnnnnnnnnn	600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnagc acatccaacc tggcttctnn nnnnnnnnnn	660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	720
nnnnnnnnnn nnnnnnnnnn nnnncagcaa agatctagtt acccactcac g	771

<210> 32
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1 protein

<400> 32	
caggtgaaac tgcagcagtc tggggcagaa cttgtgaggt cagggacctc agtcaagttg	60
tcttgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg	120
cctgaacagg gcttggagtg gattggatgg attgatcctg agaatggtga tactgaatat	180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac	240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgaggggact	300
ccgactgggc cgtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca	360
ggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgctcacc	420
cagtctccag caatcatgtc tgcactctca ggggagaagg tcaccataac ctgcagtgcc	480
agctcaagtg taagttacat gactgggttc cagcagaagc caggcacttc tcccaaactc	540
tggatttata gcacatccaa cctggcttct ggagtcctg ctcgcttcag tggcagtgga	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgccagc aaagatctag ttaccactc acgttcggtg ctggcaccaa gctggagctg	720
aaacggggcg ccacaccggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacatt	780
accccgctga tgaaagccca gtctgttcca ggcatggcgg tggccgttat ttatcaggga	840

aaaccgcact attacacatt tggcaaggcc gatatcgcg	cggaataaacc cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca	ccggcgtttt aggtggggat	960
gccattgctc gcggtgaaat ttcgctggac gatgcggtga	ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tttcgtatg ctggatctcg	ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtcacg gataacgcct	ccctgctgcg cttttatcaa	1140
aactggcagc cgcagtggaa gcctggcaca acgcgtcttt	acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcatgccct	atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggacat acctggatta	acgtgccgaa agcgggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcggtgc	gcgtttcgcc gggtatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata	tggcgaactg ggtcatggca	1440
aacatggcgc cggagaacgt tgcggatgcc tcaactaagc	agggcatcgc gctggcgcag	1500
tcgcgctact ggcgtatcgg gtcaatgtat cagggctctg	gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggt	atgtagcact ggcgccgttg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaag	cgctctgggt ccataaaacg	1680
ggctctactg gcgggtttgg cagctacgtg gcctttattc	ctgaaaagca gatcggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg	ttgaggcggc ataccatatc	1800
ctcgaggcgc tacag		1815

```

<210> 33
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRs of SW149.5 protein

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

<220>
<221> MISC_FEATURE

```

<223> X = any amino acid

<223> X = any amino acid

<223> X = any amino acid

<223> X = any amino acid

<400> 33

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		115				120						125		

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala

145		150		155		160
Ser Ser Ser Val	Ser Tyr Met His	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa				
	165		170		175	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa						
	180		185		190	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa						
	195		200		205	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln						
	210		215		220	
Arg Asp Ser Tyr Pro Leu Thr						
225		230				

<210> 34
 <211> 771
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sequence encoding CDRs of SW149.4 protein

<220>
 <221> misc_feature
 <222> (1)..(153)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (184)..(225)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (274)..(372)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (406)..(552)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (583)..(627)
 <223> n = a,t,c, or g

```

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

<400> 34
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnggcttca acattaaaga ctctatatatg      180
cacnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnntggat tgatcctgag      240
aatggtgata ctgaatatgc cccgaagttc cagnnnnnnn nnnnnnnnnn nnnnnnnnnn      300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      360
nnnnnnnnnn nngggctccc gctcggggcc atttacaacg actacnnnnn nnnnnnnnnn      420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      540
nnnnnnnnnn nnagtgccag ctcaagtgtg agttacatgc acnnnnnnnn nnnnnnnnnn      600
nnnnnnnnnn nnnnnnnnnn nnnnnnngat acatccaacc tggcttctnn nnnnnnnnnn      660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      720
nnnnnnnnnn nnnnnnnnnn nnnncagcaa agagatagtt acccactcac g              771

```

```

<210> 35
<211> 1815
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding SW149.5 protein

<400> 35
caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg      60
tcttgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg      120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatgggtga tactgaatat      180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac      240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgagggggctc      300
ccgctcgggg ccatttacia cgactactgg ggccaaggga ccacggtcac cgtctcctca      360
ggcggaggcg gttcaggcgg aggtggctct ggcgggtggcg gatcagaaaa tgtgctcacc      420
cagtctccag caatcgtgtc tgcattctca ggggagaagg tcaccataac ctgcagtgcc      480

```

agctcaagtg taagttacat gcactggttc cagcagaagc caggcacttc tcccaaactc	540
gtgatttatg atacatccaa cctggcttct ggagtccttg ctcgcttcag tggcagtgga	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgccagc aaagagatag ttaccctact acgttcggtg ctggcaccaa gctggagctg	720
aaacgggcgg ccacaccggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacgatt	780
accccgctga tgaaagccca gtctgttcca ggcatggcgg tggccgttat ttatcagggg	840
aaaccgcact attacacatt tggcaaggcc gatatcgcgg cgaataaacc cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca ccggcgtttt aggtggggat	960
gccattgctc gcggtgaaat ttcgctggac gatgcggtga ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgatatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtcacg gataacgcct ccctgctgcg cttttatcaa	1140
aactggcagc cgcagtggaa gcctggcaca acgcgtcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggg caaaccttct ggcatgcct atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggaccat acctggatta acgtgccgaa agcgggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtgc gcgtttcgcc gggtatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca	1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgag	1500
tcgcgctact ggcgtatcgg gtcaatgtat caggggtctgg gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgccgttg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaacg	1680
ggctctactg gcgggtttgg cagctacgtg gcctttatc ctgaaaagca gatcgggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata	1800
ctcgaggcgc tacag	1815

<210> 36
 <211> 1083
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sequence encoding BLA protein

 <400> 36

acaccggtgt	cagaaaaaca	gctggcggag	gtggtcgcga	atacgattac	cccgtgatg	60
aaagcccagt	ctgttccagg	catggcgggtg	gccgttat	atcagggaaa	accgcactat	120
tacacatttg	gcaaggccga	tatcgcgggc	aataaacccg	ttacgcctca	gaccctgttc	180
gagctggggt	ctataagtaa	aaccttcacc	ggcgttttag	gtggggatgc	cattgctcgc	240
ggtgaaat	cgctggacga	tgcggtgacc	agatactggc	cacagctgac	gggcaagcag	300
tggcagggta	ttcgtatgct	ggatctcgcc	acctacaccg	ctggcggcct	gccgctacag	360
gtaccggatg	aggtcacgga	taacgcctcc	ctgctgcgct	tttatcaaaa	ctggcagccg	420
cagtggaagc	ctggcacaac	gcgtctttac	gccaacgcca	gcacggtct	ttttggtgcg	480
ctggcggtca	aaccttctgg	catgcctat	gagcaggcca	tgacgacgcg	ggtccttaag	540
ccgctcaagc	tggaccatac	ctggattaac	gtgccgaaag	cggaagaggc	gcattacgcc	600
tggggctatc	gtgacggtaa	agcgggtgcgc	gtttcgccgg	gtatgctgga	tgacaagcc	660
tatggcgtga	aaaccaacgt	gcaggatatg	gcgaactggg	tcatggcaaa	catggcgccg	720
gagaacgttg	ctgatgcctc	acttaagcag	ggcatcgcgc	tggcgcagtc	gcgctactgg	780
cgtatcgggt	caatgtatca	gggtctgggc	tgggagatgc	tcaactggcc	cgtggaggcc	840
aacacggtgg	tcgagacgag	ttttggtaat	gtagcactgg	cgccgttgcc	cgtggcagaa	900
gtgaatccac	cggctcccc	ggtcaaagcg	tcctgggtcc	ataaaacggg	ctctactggc	960
gggtttggca	gctacgtggc	ctttattcct	gaaaagcaga	tcggtattgt	gatgctcgcg	1020
aatacaagct	atccgaaccc	ggcacgcgtt	gaggcggcat	accatatact	cgaggcgcta	1080
cag						1083

<210> 37
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.1 protein variant

caggtgaaac	tgacgagtc	tggggcagaa	cttgtgaaat	cagggggctc	agtcaagttg	60
tcctgcacag	cttctggctt	caacattaaa	gactcctata	tgactgggtt	gaggcagggg	120
cctgaacagg	gcctggagtg	gattggatgg	attgatcctg	agaatggtga	tactgaatat	180
gccccgaagt	tccagggcaa	ggccactttt	actacagaca	catcctccaa	cacagcctac	240
ctgcagctca	gcagcctgac	atctgaggac	actgccgtct	attattgtaa	tgaggggact	300

ccgactgggc	cgtactactt	tgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
gggtggaggcg	gttcaggcgg	aggtggctct	ggcgggtggcg	gatcagaaaa	tgtgctcacc	420
cagtctccag	caatcatgtc	tgcatctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcaagtg	taagttacat	gcactggttc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttata	gcacatccaa	cctggcttct	ggagtccttg	ctcgcttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagatctag	ttaccactc	acgttcggtg	ctggcaccaa	gctggagctg	720
aaacgggcgg	ccacaccggt	gtcagaaaaa	cagctggcgg	aggtggtcgc	gaatacgatt	780
accccgctga	tgaaagccca	gtctgttcca	ggcatggcgg	tggccgttat	ttatcaggga	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
gagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgatatg	ctggatctcg	ccacctacac	cgctggcggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	cctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaacgc	cagcatcggt	1200
ctttttggtg	cgctggcggg	caaaccttct	ggcatgccct	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcgggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggg	aaagcgggtgc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggtcatggca	1440
aacatggcgc	cggagaacgt	tgctgatgcc	tcacttaagc	agggcatcgc	gctggcgcag	1500
tcgcgctact	ggcgtatcgg	gtcaatgtat	cagggctctgg	gctgggagat	gctcaactgg	1560
cccgtggagg	ccaacacggt	ggtcgagacg	agttttggta	atgtagcact	ggcgccgttg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccggtcaaag	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcggggttgg	cagctacgtg	gcctttattc	ctgaaaagca	gatcgggtatt	1740
gtgatgctcg	cgaatacaag	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatatc	1800
ctcgaggcgc	tacag					1815

<210> 38
 <211> 605
 <212> PRT

<213> Artificial Sequence

<220>

<223> CAB1.2i protein variant

<400> 38

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
 515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
 530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
 545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
 565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
 580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
 595 600 605

<210> 39
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.2i protein variant

<400> 39
 caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
 tcttgacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120

cctgaacagg	gcctggagtg	gattggatgg	attgatcctg	agaatgggtga	tactgaatat	180
gccccgaagt	tccagggcaa	ggccactttt	actacagaca	catcctccaa	cacagcctac	240
ctgcagctca	gcagcctgac	atctgaggac	actgccgtct	attattgtaa	tgaggggact	300
ccgactgggc	cgtactactt	tgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggtggaggcg	gttcaggcgg	aggtggctct	ggcgggtggcg	gatcagaaaa	tgtgctcacc	420
cagtctccag	caatcgtgtc	tgcatctcca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcaagtg	taagttacat	gcactgggtc	cagcagaagc	caggcacttc	tcccaaactc	540
gtgatttata	gcacatccaa	cctggcttct	ggagtccctg	ctcgcttcag	tggcagtgga	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagatctag	ttaccactc	acgttcggtg	ctggcaccaa	gctggagctg	720
aaacggggcg	ccacaccggt	gtcagaaaaa	cagctggcgg	aggtggtcgc	gaatacgatt	780
accccgctga	tggcggccca	gtctgttcca	ggcatggcgg	tggccgttat	ttatcaggga	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgcgg	cgaataaacc	cgttacgcct	900
cagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	aggtggggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgtatg	ctggatctcg	ccacctacac	cgctggcggc	1080
ctgccgctac	aggtaccgga	tgaggtcacg	gataacgcct	ccctgctgcg	cttttatcaa	1140
aactggcagc	cgcagtggaa	gcctggcaca	acgcgtcttt	acgccaacgc	cagcatcggt	1200
ctttttggtg	cgctggcggt	caaaccttct	ggcatgccct	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgctcaa	gctggaccat	acctggatta	acgtgccgaa	agcggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggt	aaagcgggtgc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaactg	ggtcatggca	1440
aacatggcgc	cggagaacgt	tgctgatgcc	tcacttaagc	agggcatcgc	gctggcgcag	1500
tcgcgctact	ggcgtatcgg	gtcaatgtat	cagggctctgg	gctgggagat	gctcaactgg	1560
cccgtggagg	ccaacacggt	ggtcgagacg	agttttggta	atgtagcact	gccgccgttg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccggtcaaag	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcgggttttg	cgcgtacgtg	gcctttattc	ctgaaaagca	gatcgggtatt	1740
gtgatgctcg	cgaatacaag	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatatc	1800

ctcgaggcgc tacag

1815

<210> 40

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> CAB1.13i protein variant

<400> 40

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln

405	410	415
Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp		
420	425	430
Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg		
435	440	445
Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala		
450	455	460
Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala		
465	470	475
Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile		
485	490	495
Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly		
500	505	510
Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val		
515	520	525
Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu		
530	535	540
Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr		
545	550	555
Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys		
565	570	575
Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala		
580	585	590
Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln		
595	600	605

<210> 41
 <211> 1814
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> sequence encoding CAB1.13i protein variant

<400> 41

caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg	60
tcttgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg	120
cctgaacagg gcttggagtg gattggatgg attgatcctg agaatgggtga tactgaatat	180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac	240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgaggggctc	300
ccgctcgggg ccatttacia cgactactgg ggccaaggga ccacggtcac cgtctcctca	360
gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgctcacc	420
cagtctccag caatcgtgtc tgcattctca ggggagaagg tcaccataac ctgcagtgcc	480
agctcagctg tatatgccat gcaactggtc cagcagaagc caggcacttc tcccaaactc	540
gtgatttata gcacatccaa cctggcttct ggagtccttg ctgcgttcag tggcagtggg	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgccagc aaagagatag ttaccactc acgttcggtg ctggcaccaa gctggagctg	720
aaacgggcgg ccacaccggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacgatt	780
accccgctga tggcgggcca gtctgttcca ggcatggcgg tggccgttat ttatcagggg	840
aaaccgcact attacacatt tggcaaggcc gatatcgcg cgaataaacc cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca ccggcgtttt ggtggggatg	960
ccattgctcg cgggtgaaatt tcgctggacg atgcggtgac cagatactgg ccacagctga	1020
cgggcaagca gtggcagggg attcgtatgc tggatctcgc cacctacacc gctggcggcc	1080
tgccgctaca ggtaccgat gaggtcacgg ataacgcctc cctgctgcgc ttttatcaaa	1140
actggcagcc gcagtggaag cctggcacia cgcgtcttta cgccaacgcc agcatcggtc	1200
tttttggtgc gctggcggtc aaaccttctg gcatgccta tgagcaggcc atgacgacgc	1260
gggtccttaa gccgctcaag ctggaccata cctggattaa cgtgccgaaa gcggaagagg	1320
cgcattacgc ctggggctat cgtgacggta aagcggtgcg cgtttcgccg ggtatgctgg	1380
atgcacaagc ctatggcgtg aaaaccaacg tgcaggatat ggccaactgg gtcattggcaa	1440
acatggcgcc ggagaacgtt gctgatgcct cacttaagca gggcatcgcg ctggcgagct	1500
cgcgctactg gcgtatcggg tcaatgtatc agggctctgg ctgggagatg ctcaactggc	1560
ccgtggaggc caacacggtg gtcgagacga gttttggtaa tgtagcactg gcgccgttgc	1620

ccgtggcaga agtgaatcca ccggctcccc cgggtcaaagc gtctctgggtc cataaaacgg 1680
gctctactgg cggggtttggc gcgtacgtgg cctttattcc tgaaaagcag atcggtattg 1740
tgatgctcgc gaatacaagc tatccgaacc cggcacgcgt tgaggcggca taccatatcc 1800
tcgaggcgct acag 1814

<210> 42
<211> 623
<212> PRT
<213> Artificial Sequence
<220>
<223> CAB1.13i protein variant
<400> 42

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Val	Ser	Leu	Gly
1				5					10					15	
Gln	Arg	Ala	Thr	Met	Ser	Cys	Arg	Ala	Gly	Glu	Ser	Val	Asp	Ile	Phe
			20					25					30		
Gly	Val	Gly	Phe	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro
		35					40					45			
Lys	Leu	Leu	Ile	Tyr	Arg	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Val
	50					55					60				
Arg	Phe	Ser	Gly	Thr	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ile	Ile	Asp
65					70					75					80
Pro	Val	Glu	Ala	Asp	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Thr	Asn
				85					90					95	
Glu	Asp	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly
		100						105					110		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
		115					120					125			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln
	130					135					140				
Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Glu	Pro	Gly	Ala	Ser	Val	Lys
145					150					155					160

Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
165 170 175

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
180 185 190

Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
195 200 205

Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
210 215 220

Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225 230 235 240

Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
245 250 255

Ser Val Thr Val Ser Ser Thr Pro Val Ser Glu Lys Gln Leu Ala Glu
260 265 270

Val Val Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro
275 280 285

Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr
290 295 300

Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr
305 310 315 320

Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly
325 330 335

Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr
340 345 350

Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met
355 360 365

Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro
370 375 380

Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp
385 390 395 400

Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser
405 410 415

Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr
420 425 430

Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His
435 440 445

Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly
450 455 460

Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala
465 470 475 480

Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val
485 490 495

Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln
500 505 510

Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr
515 520 525

Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr
530 535 540

Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val
545 550 555 560

Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His
565 570 575

Lys Thr Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro
580 585 590

Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn
595 600 605

Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
610 615 620

<210> 43
<211> 1869
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CAB1.11i protein variant

<400> 43
gacatcgtcc tgacccagag cccggcaagc ctgtctgttt ccctgggcca gcgtgccact 60
atgtcctgca gagcgggtga gtctgttgac attttcggtg tcggttttct gcactggtac 120
caacagaaac cgggtcagcc gccaaaactg ctgatctatc gtgcttctaa cctggagtc 180
ggcatcccggt tacgtttctc cgggtactggc tctggtactg attttaccct gattatcgac 240
ccggtggaag cagacgatgt tgccacctac tattgccagc agaccaacga ggatccgtac 300
accttcggtg gcggtactaa actggagatc aaaggcgggtg gtggttctgg tgggtggtggt 360
agcggtgggc gtggtagcgg tggcgggtggc agcggtggtg gtggctctgg tggcgggtggc 420
tctgaagtgc agctgcagca gtccgggtgcg gagctcggtt aaccgggcgc ttctgtgaaa 480
ctgtcttgca ctgcatctgg tttcaacatt aaggacacct acatgcactg ggtgaaacaa 540
cgcccgaac aggggtctgga gtggatcgggt cgcctcgatc cggctaacgg taacagcaaa 600
tacgtgcaa aattccaggg taaagcaacc atcactgctg atacctcctc taacactgct 660
tacctgcagc tgacttcctc gactagcgaa gacaccggc tttattactg cgctccgttc 720
ggctactatg tcagcgatta cgcaatggcc tactgggggtc agggcacctc tgttaccgtt 780
tctagcacac cgggtgtcaga aaaacagctg gcggaggtgg tcgcgaatac gattaccccg 840
ctgatggcgg ccagctctgt tccaggcatg gcggtggccg ttatttatca gggaaaaccg 900
cactattaca catttgcaa ggccgatatc gcggcgaaata aaccggttac gcctcagacc 960
ctgttcgagc tgggttctat aagtaaaacc ttcaccggcg ttttaggtgg ggatgccatt 1020
gctcgcggtg aaatttcgct ggacgatgcg gtgaccagat actggccaca gctgacgggc 1080
aagcagtggc agggatttcg tatgctggat ctcgccacct acaccgctgg cggcctgccg 1140
ctacaggtac cggatgaggt cacggataac gcctccctgc tgcgctttta tcaaaactgg 1200
cagccgcagt ggaagcctgg cacaacgcgt ctttacgcca acgccagcat cggctctttt 1260
ggtgcgctgg cgggtcaaacc ttctggcatg ccctatgagc aggccatgac gacgcgggtc 1320

cttaagccgc tcaagctgga ccatacctgg attaacgtgc cgaaagcgga agagggcgcat	1380
tacgcctggg gctatcgtga cggtaaagcg gtgcgcgttt cgccgggtat gctggatgca	1440
caagcctatg gcgtgaaaac caacgtgcag gatatggcga actgggtcat ggcaaactg	1500
gcgcgggaga acgttgctga tgcctcactt aagcagggca tcgcgctggc gcagtcgcgc	1560
tactggcgta tcgggtcaat gtatcagggg ctgggctggg agatgctcaa ctggcccgtg	1620
gaggccaaca cgggtggtcga gacgagtttt ggtaatgtag cactggcgcc gttgcccgtg	1680
gcagaagtga atccaccggc tcccccggtc aaagcgtcct ggggccataa aacgggctct	1740
actggcgggt ttggcgcgta cgtggccttt attcctgaaa agcagatcgg tattgtgatg	1800
ctcgcgaata caagctatcc gaaccggca cgcgttgagg cggcatacca tatectcgag	1860
gcgctacag	1869

<210> 44
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 44	
cggccatggc ccaggtgcag ctgcagcagt ctggggc	37

<210> 45
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 45	
ctggggcaga acttgtgaaa tcagggacct cagtcaa	37

<210> 46
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 46	
gggcagaact tgtgaggccg gggacctcag tcaagtt	37

<210> 47
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 47
 aacttgtgag gtcagggggc tcagtcaagt tgtcctg 37

<210> 48
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 48
 gcacagcttc tggcttcacc attaaagact cctatat 37

<210> 49
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 49
 cagcttctgg cttcaacttt aaagactcct atatgca 37

<210> 50
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 50
 cttctggctt caacattagc gactcctata tgcactg 37

<210> 51
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 51

actcctatat gcactgggtg aggcaggggc ctgaaca 37

<210> 52
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 52
tgcactgggtt gaggcaggcg cctgaacagg gcctgga 37

<210> 53
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 53
ggttgaggca ggggcctggc cagggcctgg agtggat 37

<210> 54
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 54
ccccgaagtt ccagggccgt gccactttta ctacaga 37

<210> 55
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 55
cgaagttcca gggcaagttc acttttacta cagacac 37

<210> 56
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 56

tccagggcaa ggccactatt actacagaca catcctc

37

<210> 57

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 57

gcaaggccac ttttactcgc gacacatcct ccaacac

37

<210> 58

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 58

ttactacaga cacatccaaa aacacagcct acctgca

37

<210> 59

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 59

ctgccgtcta ttattgtgcg gaggggactc cgactgg

37

<210> 60

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 60

ccgtctatta ttgtaatcgc gggactccga ctgggcc

37

<210> 61

<211> 37

<212> DNA

<213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 61
 ctggcgggtgg cggatcacag aatgtgctca cccagtc 37

<210> 62
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 62
 gcggtggcgg atcagaaagc gtgctcaccc agtctcc 37

<210> 63
 <211> 38
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 63
 gaaaatgtgc tcaccagcc gccagcaatc atgtctgc 38

<210> 64
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 64
 tgctcaccca gtctccaagc atcatgtctg catctcc 37

<210> 65
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 65
 cccagtctcc agcaatcgtg tctgcatctc cagggga 37

<210> 66
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 66
 tgtctgcatc tccagggcag aaggtcacca taacctg 37

<210> 67
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 67
 ctgcatctcc aggggagacc gtcaccataa cctgcag 37

<210> 68
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 68
 taagttacat gcactggtac cagcagaagc caggcac 37

<210> 69
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 69
 gcacttctcc caaactcgtg atttatagca catccaa 37

<210> 70
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 70

tggtttctgg agtccctgat cgcttcagtg gcagtgg 37

<210> 71
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 71
ctcgcttcag tggcagtaaa tctgggacct cttactc 37

<210> 72
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 72
gtggatctgg gacctctgcg tctctcacia tcagccg 37

<210> 73
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 73
ctctcacaat cagccgactg gaggctgaag atgctgc 37

<210> 74
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 74
gaatggaggc tgaagatgaa gccacttatt actgcc 37

<210> 75
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 75
aggctgaaga tgctgccgat tattactgcc agcaaag

37

<210> 76
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 76
accactcac gttcggtggc ggcaccaagc tggagct

37

<210> 77
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 77
cttctggctt caacattsat gactcctata tgcactg

37

<210> 78
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 78
ctggcttcaa cattaaasat tcctatatgc actgggt

37

<210> 79
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79
gcttcaacat taaagacsat tatatgcact gggtag

37

<210> 80
<211> 37
<212> DNA

<213> Artificial Sequence
 <220>
 <223> primer
 <400> 80
 tcaacattaa agactccsat atgcactggg tgaggca 37
 <210> 81
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 81
 ttaaagactc ctatatgsat tgggtgaggc aggggcc 37
 <210> 82
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 82
 gcctggagtg gattggasat attgacctg agaatgg 37
 <210> 83
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 83
 agtggattgg atggattsat cctgagaatg gtgatac 37
 <210> 84
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 84
 ttggatggat tgatcctsat aatggtgata ctgaata 37

<210> 85
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 85
gatggattga tcctgagsat ggtgatactg aatatgc

37

<210> 86
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 86
ttgatcctga gaatggsat actgaatatg ccccgaa

37

<210> 87
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 87
atcctgagaa tggtgatsat gaatatgcc cgaagtt

37

<210> 88
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 88
ctgagaatgg tgatactsat tatgccccga agttcca

37

<210> 89
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 89

gtgataactga atatgccsat aagttccagg gcaaggc 37

<210> 90
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 90
atactgaata tgccccgsat ttccagggca aggccac 37

<210> 91
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 91
aatatgcccc gaagttcsat ggcaaggcca cttttac 37

<210> 92
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 92
ccgtctatta ttgtaatsat gggactccga ctgggcc 37

<210> 93
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 93
tctattattg taatgagsat actccgactg ggccgta 37

<210> 94
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 94
attattgtaa tgaggggsat ccgactgggc cgtacta

37

<210> 95
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 95
attgtaatga ggggactsat actgggccgt actactt

37

<210> 96
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 96
gtaatgaggg gactccgsat gggccgtact actttga

37

<210> 97
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 97
atgaggggac tccgactsat ccgtactact ttgacta

37

<210> 98
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 98
aggggactcc gactgggsat tactactttg actactg

37

<210> 99
<211> 37
<212> DNA

<213> Artificial Sequence
 <220>
 <223> primer
 <400> 99
 ctccgactgg gccgtacsat ttgactact ggggccca 37

<210> 100
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 100
 taacctgcag tgccagcsat agtgtaagtt acatgca 37

<210> 101
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 101
 cctgcagtgc cagctcasat gtaagttaca tgcactg 37

<210> 102
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 102
 gcagtgccag ctcaagtsat agttacatgc actgggt 37

<210> 103
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 103
 gtgccagctc aagtgtasat tacatgcact ggttcca 37

<210> 104
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 104
 ccagctcaag tgtaagtsat atgcactggg tccagca 37

<210> 105
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 105
 ctcccaaact cgtgattsat agcacatcca acctggc 37

<210> 106
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 106
 ccaaactcgt gatttatsat acatccaacc tggcttc 37

<210> 107
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 107
 aactcgtgat ttatagcsat tccaacctgg cttctgg 37

<210> 108
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 108

tcgtgattta tagcacasat aacctggctt ctggagt 37

<210> 109
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 109
tgatttatag cacatccsat ctggcttctg gagtccc 37

<210> 110
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 110
atagcacatc caacctgsat tctggagtcc ctgctcg 37

<210> 111
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 111
gcacatccaa cctggctsat ggagtccttg ctcgctt 37

<210> 112
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 112
cttattactg ccagcaasat tctagttacc cactcac 37

<210> 113
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 113

attactgcca gcaaagasat agttacccac tcacgt

36

<210> 114

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 114

actgccagca aagatctsat taccactca cgttcg

36

<210> 115

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 115

gccagcaaag atctagtsat ccactcacgt tcggtg

36

<210> 116

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 116

aaagatctag ttacccasat acgttcggtg ctggcac

37

<210> 117

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 117

caggaaacag ctatgac

17

<210> 118

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 118

ggaccacggg caccgtctcc tc

22

<210> 119

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<220>

<221> misc_feature

<222> (18)..(19)

<223> n = a,t,c, or g

<400> 119

attattgtaa tgaggggnns ccgactgggc cgtacta

37

<210> 120

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<220>

<221> misc_feature

<222> (19)..(20)

<223> n = a,t,c, or g

<400> 120

tagtacggcc cagtcggsnn cccctcatta caataat

37

<210> 121

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (18)..(19)

<223> n = a,t,c, or g

<400> 121

gtaatgaggg gctgccgnns gggccgtact actttga

37

<210> 122

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (19)..(20)

<223> n = a,t,c, or g

<400> 122

tcaaagtagt acggcccsnn cggcagcccc tcattac

37

<210> 123

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (18)..(19)

<223> n = a,t,c, or g

<400> 123

cgactgggcc gtactacnns gactactggg gccaaagg

37

<210> 124

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (19)..(20)

<223> n = a,t,c, or g

<400> 124

ccttggtcccc agtagtcsnn gtagtacggc ccagtcg

37

<210> 125
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (22)..(22)
<223> n = a,t,c, or g

<400> 125
gaggggtccc cgctcggrv cntttacaac gactactggg gccaaagg

47

<210> 126
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (26)..(26)
<223> n = a,t,c, or g

<400> 126
ccttggtcccc agtagtcgtt gtaaangbyc ccgagcggga gcccttc

47

<210> 127
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 127
cttctggctt caacattacc gactcctata tgcactg

37

<210> 128
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 128

gcctggagtg gattggattt attgacctg agaatg

36

<210> 129

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (41)..(41)

<223> n = a,t,c, or g

<400> 129

gacctgaga atggtswtrc tgaatatgcc cbgaagttrc ncggcaaggc cacttttac

59

<210> 130

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 130

ctgcagtgcc agctcadctg taymtdccat gcactgggtc cagc

44

<210> 131

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 131

cgtgatttat gatacarvca acctggctrs tggagtcctt gctcgcttc

49

<210> 132

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 132

gattaccccg ctgatggcgg cccagtctgt tccag

35

<210> 133

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 133

ctactggcgg gtttggcgcg tacgtggcct ttattcctg

39